

Detail Description Paragraph:

[0045] The terms ".alpha.-1,3/4-fucosyltransferase or fucosyltransferase" or a nucleic acid encoding an ".alpha.-1,3/4-fucosyltransferase or fucosyltransferase" refer to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to a polypeptide encoded by a nucleic acid selected from SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:19; or an amino acid sequence of SEQ ID NO:2; SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, or SEQ ID NO:20; (2) specifically bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of SEQ ID NO:2; SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, or SEQ ID NO:20; immunogenic fragments thereof, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid encoding SEQ ID NO:2; SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, or SEQ ID NO:20; e.g., a nucleic acid sequence of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:19; or its complement, and conservatively modified variants thereof; (4) have a nucleic acid sequence that has greater than about 90%, preferably greater than about 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, or SEQ ID NO:19; or its complement. The nucleic acids and proteins of the invention include both naturally occurring or recombinant molecules.

```

<!--StartFragment-->RESULT 4
ADJ77816
ID  ADJ77816 standard; protein; 277 AA.
XX
AC  ADJ77816;
XX
DT  06-MAY-2004 (first entry)
XX
DE  Helicobacter pylori strain 19C2 FutB protein SeqID 8.
XX
KW  FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
KW  fucose; N-acetylglucosamine; glycoconjugate; enzyme.
XX
OS  Helicobacter pylori.
XX
PN  WO2004009838-A2.
XX
PD  29-JAN-2004.
XX
PF  23-JUL-2003; 2003WO-US023057.
XX
PR  23-JUL-2002; 2002US-0398156P.
PR  08-NOV-2002; 2002US-0424894P.
XX
PA  (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI  Johnson KF, Bezila DJ;
XX
DR  WPI; 2004-123401/12.
DR  N-PSDB; ADJ77815.
XX
PT  New isolated polynucleotide encoding fucosyltransferase protein, useful
PT  for synthesizing oligosaccharide moiety on a protein or lipid that is
PT  unglycosylated in its native form or for synthesizing glycolipids.
XX
PS  Claim 16; SEQ ID NO 8; 72pp; English.
XX
CC  This invention relates to novel isolated polynucleotides and the encoded
CC  polypeptides thereof, which are related to the fucosyltransferase enzymes
CC  (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
CC  refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
CC  chemically synthesise glycoproteins and glycolipids with the desired
CC  oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
CC  acetylglucosamine), such that they are useful in the preparation of
CC  glycoconjugates. The present invention describes how bacterial
CC  fucosyltransferase is unaffected by the sialylation status of the acceptor
CC  sugar, as opposed to the mammalian homologue, and furthermore,
CC  bacterially expressed enzymes offer a large cost saving relative to
CC  mammalian expression systems. This polypeptide sequence is an H. pylori
CC  strain 19C2 FutB protein sequence of the invention.
XX
SQ  Sequence 277 AA;

Query Match          15.2%; Score 68; DB 8; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.5e-57;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 NPLGSARKILSYQNAKRVFYTGGENEVPNFDYAIGFDELDFRDRYLRMPPLYDRLHHK 132
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 74 NPLGSARKILSYQNAKRVFYTGGENEVPNFDYAIGFDELDFRDRYLRMPPLYDRLHHK 133

```

Qy 133 AESVNDTT 140
 | | | | | | | |
Db 134 AESVNDTT 141

<!--EndFragment-->

<!--StartFragment-->RESULT 5

ADJ27351

ID ADJ27351 standard; protein; 277 AA.

XX

AC ADJ27351;

XX

DT 20-MAY-2004 (first entry)

XX

DE Alpha-1,3/4-fucosyltransferase coding sequence.

XX

KW alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;

KW fucosyl; fucose.

XX

OS Helicobacter pylori; strain 19C2 FutB.

XX

PN WO2004009793-A2.

XX

PD 29-JAN-2004.

XX

PF 23-JUL-2003; 2003WO-US023155.

XX

PR 23-JUL-2002; 2002US-0398156P.

PR 08-NOV-2002; 2002US-0424894P.

XX

PA (NEOS-) NEOSE TECHNOLOGIES INC.

XX

PI Johnson KF, Bezila DJ;

XX

DR WPI; 2004-132958/13.

DR N-PSDB; ADJ27350.

XX

PT Producing fucosylated glycoprotein, by contacting recombinant

PT fucosyltransferase protein with mixture comprising donor substrate and

PT acceptor substrate on glycoprotein.

XX

PS Claim 1; Fig 4; 84pp; English.

XX

CC This sequence represents an alpha-1,3/4-fucosyltransferase protein which
 CC was used in the method of the invention for producing a fucosylated
 CC glycoprotein. The method involves contacting a recombinant
 CC fucosyltransferase protein with a mixture comprising a donor substrate
 CC which comprises a fucosyl residue, and an acceptor substrate on a
 CC glycoprotein, under conditions such that the fucosyltransferase protein
 CC catalyzes the transfer of the fucose residue from a donor substrate to
 CC the acceptor substrate on the glycoprotein. The method is useful for
 CC producing fucosylated glycoprotein.

XX

SQ Sequence 277 AA;

Query Match 15.2%; Score 68; DB 8; Length 277;

Best Local Similarity 100.0%; Pred. No. 1.5e-57;

Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 NPLGSARKILSYQNAKRVFYTGNEVPNFNLFDYAIGFDELDFRDRYLRMPLYDRLHHK 132

|||||

Db 74 NPLGSARKILSYQNAKRVFYTGNEVPNFNLFDYAIGFDELDFRDRYLRMPLYDRLHHK 133

Qy 133 AESVNDTT 140

|||||

Db 134 AESVNDTT 141

<!--EndFragment-->

<!--StartFragment-->RESULT 7

ADJ77810

ID ADJ77810 standard; protein; 486 AA.

XX

AC ADJ77810;

XX

DT 06-MAY-2004 (first entry)

XX

DE Helicobacter pylori strain 1182 FutB protein SeqID 2.

XX

KW FutA; FutB; alpha 1-3/4 fucosyltransferase; glycoprotein; glycolipid;
KW fucose; N-acetylglucosamine; glycoconjugate; enzyme.

XX

OS Helicobacter pylori.

XX

PN WO2004009838-A2.

XX

PD 29-JAN-2004.

XX

PF 23-JUL-2003; 2003WO-US023057.

XX

PR 23-JUL-2002; 2002US-0398156P.

PR

08-NOV-2002; 2002US-0424894P.

XX

PA (NEOS-) NEOSE TECHNOLOGIES INC.

XX

PI Johnson KF, Bezila DJ;

XX

DR WPI; 2004-123401/12.

DR

N-PSDB; ADJ77809.

XX

PT New isolated polynucleotide encoding fucosyltransferase protein, useful

PT for synthesizing oligosaccharide moiety on a protein or lipid that is

PT unglycosylated in its native form or for synthesizing glycolipids.

XX

PS Claim 16; SEQ ID NO 2; 72pp; English.

XX

CC This invention relates to novel isolated polynucleotides and the encoded
 CC polypeptides thereof, which are related to the fucosyltransferase enzymes
 CC (FutA and FutB) of Helicobacter pylori (H. pylori). Specifically, it
 CC refers to alpha 1-3/4 fucosyltransferase enzymes that can be used to
 CC chemically synthesise glycoproteins and glycolipids with the desired
 CC oligosaccharide moieties (i.e. by transfer of a fucose residue to N-
 CC acetylglucosamine), such that they are useful in the preparation of
 CC glycoconjugates. The present invention describes how bacterial
 CC fucosyltransferase is unaffected by the sialylation status of the acceptor
 CC sugar, as opposed to the mammalian homologue, and furthermore,
 CC bacterially expressed enzymes offer a large cost saving relative to
 CC mammalian expression systems. This polypeptide sequence is an H. pylori
 CC strain 1182 FutB protein sequence of the invention.

XX

SQ Sequence 486 AA;

Query Match 13.2%; Score 59; DB 8; Length 486;

Best Local Similarity 100.0%; Pred. No. 1.6e-48;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 366 DDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYERLLQNASPLLELSQNT 424

|||||

Db 400 DDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYERLLQNASPLLELSQNT 458

<!--EndFragment-->

```

<!--StartFragment-->ADJ27345
ID  ADJ27345 standard; protein; 486 AA.
XX
AC  ADJ27345;
XX
DT  20-MAY-2004 (first entry)
XX
DE  Alpha-1,3/4-fucosyltransferase.
XX
KW  alpha-1; 3/4-fucosyltransferase; glycoprotein; fucosyltransferase;
KW  fucosyl; fucose.
XX
OS  Helicobacter pylori; strain 1182 FutB.
XX
PN  WO2004009793-A2.
XX
PD  29-JAN-2004.
XX
PF  23-JUL-2003; 2003WO-US023155.
XX
PR  23-JUL-2002; 2002US-0398156P.
PR  08-NOV-2002; 2002US-0424894P.
XX
PA  (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI  Johnson KF, Bezila DJ;
XX
DR  WPI; 2004-132958/13.
DR  N-PSDB; ADJ27344.
XX
PT  Producing fucosylated glycoprotein, by contacting recombinant
PT  fucosyltransferase protein with mixture comprising donor substrate and
PT  acceptor substrate on glycoprotein.
XX
PS  Claim 1; Fig 1; 84pp; English.
XX
CC  This sequence represents an alpha-1,3/4-fucosyltransferase protein which
CC  was used in the method of the invention for producing a fucosylated
CC  glycoprotein. The method involves contacting a recombinant
CC  fucosyltransferase protein with a mixture comprising a donor substrate
CC  which comprises a fucosyl residue, and an acceptor substrate on a
CC  glycoprotein, under conditions such that the fucosyltransferase protein
CC  catalyzes the transfer of the fucose residue from a donor substrate to
CC  the acceptor substrate on the glycoprotein. The method is useful for
CC  producing fucosylated glycoprotein.
XX
SQ  Sequence 486 AA;

Query Match          13.2%; Score 59; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      366 DDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYERLLQNASPLLELSQNT 424
          |||
Db      400 DDLRVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYDDL RVNYERLLQNASPLLELSQNT 458
<!--EndFragment-->

```